

Amendments to the Specification:

Please insert the paper copy of the Sequence Listing filed herewith following the Oath/Declaration.

Please replace paragraph [0025] beginning at page 6 as with the following amended paragraph:

[0025] Figure 6 is the amino acid sequence of KCHIP-1 that was expressed in E. coli and used for crystallization. The sequence shown includes KCHIP-1, with two additional amino acids (i.e., Val and Glu) and six His-tag at the C-terminal (SEQ ID NO:1).

Please replace paragraph [0026] beginning at page 6 as with the following amended paragraph:

[0026] Figure 7 is the amino acid sequence of the T1 domain of Kv4.3 that was expressed in E. coli and used for crystallization. The sequence shown includes Kv4.3 T1, with one additional amino acid (i.e., Met) at the N-terminal, and two additional amino acids (i.e., Leu and Glu) and six His-tag at the C-terminal (SEQ ID NO:2).

Please replace paragraph [0064] beginning at page 19 as with the following amended paragraph:

[0064] *Overall Structure - Kv4.3 T1.* The structure of the T1 monomer can be seen as consisting of two sub-domains or four layers (Figure 2). These four layers are stacked along the four-fold axis of the homotetramer of T1. The N- and C-termini of each subunit are placed at opposite faces of the tetramer. The N-terminal layer 1 (38-85) is formed by two pairs of antiparallel β -strands interrupted by two short α -helices (one is distorted) between them. The two pairs of β -strands interact in parallel fashion to form a four-stranded β -sheet of layer 1. The following layer 2 consists of a single 15-residue long α -helix (86-101). A β -strand and an α -helix (102-123) form layer 3 of the structure. C-terminal layer 4 has a turn and a long 17-residue

α -helix, which binds a Zn^{2+} with layer 3. There is one Zn^{2+} per monomer, which is tetrahedrally coordinated by Cys 131 and Cys 132 from layer 4, His 104 from layer 3, and a single cysteine (Cys 110) from layer 3 of the adjacent monomer (Figure 2 & 3). The $\text{HX}_5\text{CX}_{20}\text{CC Zn}^{2+}$ binding motif (SEQ ID NO:3) is conserved in *Shal*, *Shaw* or *Shab* channels. An apparent function for the Zn^{2+} is to confer the conformation of layer 4 and promote inter-subunit contacts. The Zn^{2+} may also play an important role in differentiating *Shad*, *Shal* or *Shaw* like channels from *Shaker* like T1 in assembly, since the Zn^{2+} binding sequence motif and Zn^{2+} are not present in *Shaker* like channels.